Barley stem rust resistance genes: cloning, structure and mechanism of action

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The barley stem rust resistance genes *Rpg1*, providing resistance to many *Puccinia graminis* f. sp. *tritici* pathotypes, and *Rpg5,* providing resistance to *Puccinia graminis* f. sp. *secalis* pathotype 92-MN-90, were cloned and characterized. The in silico translated RPG1 protein consists of tandem serine/threonine protein kinase (PK) domains, but only the C terminal domain is an active kinase while the N terminal domain is a pseudokinase. The predicted RPG5 protein consists of NBS-LRR-PK domains and thus represents a unique structure where the nucleotide binding site and leucine rich repeat domains are fused with the protein kinase domain in a single gene. The *rpg4* gene remains a mystery, but the analysis of recombinants strongly suggests that it is and Actin Depolymerizing Factor gene. It appears that the *rpg4*-mediated resistance to pathotype QCC requires the presence of the *Rpg5* gene. The pathotype Ug99 resistance gene maps to the *Rpg5/rpg4* complex locus and may be the same as *Rpg5* (Steffenson, this workshop). Mutant analysis indicated that an active protein kinase domain is essential for *Rpg1*-mediated disease resistance. However, the pseudokinase domain also provides an essential, although so far unknown function essential for disease resistance. Surprisingly, the RPG1 protein is degraded within 20 - 24 hrs. after infection by avirulent, but not by virulent, stem rust pathotypes. Mutant analysis suggests that the degradation of the RPG1 protein appears to be essential, but not sufficient, for disease resistance.